

Please enter the following amendments and remarks.

Listing of the claims:

What is claimed is:

1. - 44. (Canceled)

45. (Currently amended) A method for detecting coronary artery disease in a human test subject, said method comprising:

a) ~~Quantifying in RNA of a blood sample from said test subject,~~ a level of RNA encoded by ~~the gene an~~ ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1) gene in said a blood sample of said test subject; and

b) ~~Comparing said quantified level of RNA in said sample of said test subject with a~~ quantified level of control RNA encoded by said gene in ~~RNA of blood samples from~~ control subjects which are classified as healthy control subjects; and

c) comparing said level of RNA in said sample of said test subject a quantified level of control RNA encoded by said gene in blood samples of control subjects which are classified as having coronary artery disease;

wherein ~~said comparison of a statistically significant determination resulting from steps (b) and (c) that expression of said quantified level of step (a) with gene in said sample of said test subject is different relative to said quantified level of said samples of said control RNA classified as healthy control subjects, and is similar relative to said samples of said control subjects classified as having coronary artery disease~~ is indicative of coronary artery disease in said human test subject.

46. (Currently amended) The method of claim 45, wherein said blood sample of ~~step (a)~~ said test subject and said blood samples ~~from~~ said control subjects ~~in step (b)~~ have not been fractionated into cell types.

47. (Cancelled) ~~The method of claim 45, wherein said blood sample of step (a) and said blood samples from said control subjects in step (b) are unfractionated samples of lysed blood.~~

48. (Currently amended) The method of ~~any of claims 45, 46 or 47~~56, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene in said sample of said test subject in step (a) is effected ~~by quantifying said RNA~~ relative to a housekeeping gene.

49. (Currently amended) The method of ~~any of claims 45, 46 or 47~~56, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene in said sample of said test subject in step (a) is effected by quantification of cDNA ~~corresponding~~ complementary to said RNA encoded by said gene.

50. (Cancelled) ~~The method of any of claims 45, 46 or 47, wherein said control subjects do not have coronary artery disease and said comparison of step (b) results in a statistically significant difference.~~

51. (Cancelled) ~~The method of any of claims 45, 46 or 47, wherein said control subjects have been diagnosed as having coronary artery disease and said comparison results in a statistically significant similarity.~~

52. (Currently Amended) The method of ~~any of claims 45 or claim 56, 46 or 47~~, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene ~~in step (a)~~ is ~~determined~~ effected using quantitative ~~real-time~~ RT-PCR.

53. (Currently amended) The method of ~~any of claims 45 or claim 56, 46 or 47~~, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene ~~in step (a)~~ is ~~determined~~ effected using an array.

54. (New) A method for detecting expression of an ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1) gene in a human test subject, said method comprising detecting RNA

encoded by said gene in a blood sample of said test subject, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene in said sample, and/or for cDNA complementary to RNA encoded by said gene in said sample.

55. (New) The method of claim 54, wherein said detecting of said RNA comprises producing an amplification product from RNA encoded by said gene in said blood sample of said test subject, using primers specific only for RNA encoded by said gene and/or for cDNA complementary to RNA encoded by said gene.

56. (New) The method of claim 54 or claim 55, further comprising quantifying a level of RNA encoded by said gene in said sample.

57. (New) The method of claim 56, further comprising comparing said level of RNA to a quantified level of control RNA encoded by said gene in blood samples of control subjects.

58. (New) The method of claim 57, wherein said control subjects are selected from the group consisting of: subjects classified as healthy subjects and subjects classified as having coronary artery disease.

59. (New) The method of claim 58, wherein said control subjects are classified as healthy subjects.

60. (New) The method of claim 59, further comprising classifying said test subject as being a candidate for having coronary artery disease if said level of RNA encoded by said gene in said blood sample of said human test subject is lower than that of said control subjects classified as healthy subjects.

61. (New) The method of claim 59, further comprising identifying said test subject as being a candidate for having coronary artery disease if said level of RNA encoded by said gene in said blood sample of said human test subject is at least 1.5 times lower than that of said control subjects classified as healthy subjects.

62. (New) The method of claim 59, further comprising identifying said test subject as being a candidate for having coronary artery disease if said level of RNA encoded by said gene in said blood sample of said human test subject is 1.54 times lower than that of said control subjects classified as healthy subjects.
63. (New) The method of claim 61, wherein said gene is differentially expressed in said blood sample of said human test subject relative to said samples of said control subjects classified as healthy subjects with a p value less than 0.05.
64. (New) The method of claim 62, wherein said gene is differentially expressed in said blood sample of said human test subject relative to said samples of said control subjects classified as healthy subjects with a p value equal to 0.0001.
65. (New) A method of screening a human test subject for being a candidate for having coronary artery disease, said method comprising:
- (a) detecting RNA encoded by an ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1) gene in a blood sample of said test subject, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene in said sample, and/or for cDNA complementary to RNA encoded by said gene in said sample; and
 - (b) quantifying a level of RNA encoded by said gene in said sample of said test subject; and
 - (c) comparing said level of RNA in said sample of said test subject to a quantified level of control RNA encoded by said gene in blood samples of control subjects classified as healthy subjects;
- wherein said test subject is a candidate for having coronary artery disease if said level of RNA encoded by said gene in said blood sample of said test subject is at least 1.5 times lower than said level of RNA encoded by said gene in said samples of said control subjects classified as healthy subjects with a p value less than 0.05.

66. (New) A method of screening a human test subject for being a candidate for having coronary artery disease, said method comprising:

(a) detecting RNA encoded by an ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1) gene in a blood sample of said test subject, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene in said sample, and/or for cDNA complementary to RNA encoded by said gene in said sample; and

(b) quantifying a level of RNA encoded by said gene in said sample; and

(c) comparing said level of RNA in said sample of said test subject to a quantified level of control RNA encoded by said gene in blood samples of control subjects classified as healthy subjects;

wherein said test subject is a candidate for having coronary artery disease if said level of RNA encoded by said gene in said blood sample of said human test subject is 1.54 times lower than said level of RNA encoded by said gene in said samples of said control subjects classified as healthy subjects with a p value equal to 0.0001.

67. (New) The method of claim 54 or claim 55, wherein said blood sample is selected from the group consisting of: a whole blood sample, a blood sample which has not been fractionated into cell types, and a blood sample which comprises leukocytes which have not been fractionated into cell types.

68. (New) The method of claim 56, wherein said blood sample is selected from the group consisting of: a whole blood sample, a blood sample in which has not been fractionated into cell types, and a blood sample which comprises leukocytes which have not been fractionated into cell types.

69. (New) The method of claim 57, wherein:

(i) said blood sample of said test subject and said blood samples of said control subjects are whole blood samples; or

(ii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which have not been fractionated into cell types; or

(iii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which comprise leukocytes which have not been fractionated into cell types.

70. (New) The method of claim 65 or claim 66, wherein:

(i) said blood sample of said test subject and said blood samples of said control subjects are whole blood samples; or

(ii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which have not been fractionated into cell types; or

(iii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which comprise leukocytes which have not been fractionated into cell types.

71. (New) A method of identifying an ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1) gene as a candidate biomarker for coronary artery disease in a human subject, said method comprising:

(a) detecting RNA encoded by said gene in blood samples of human patients diagnosed as having coronary artery disease, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene in said samples, and/or for cDNA complementary to RNA encoded by said gene in said samples; and

(b) quantifying a level of RNA encoded by said gene in said samples; and

(c) comparing said level to a quantified level of control RNA encoded by said gene in blood samples of healthy control subjects;

wherein said gene is a candidate biomarker for coronary artery disease in a human subject if said level of RNA encoded by said gene in said samples of said human patients diagnosed as having coronary artery disease is at least 1.5 times lower than said level of RNA encoded by said gene in said samples of said healthy subjects with a p value less than 0.05.

72. (New) A method of identifying an ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1) gene as a candidate biomarker for coronary artery disease in a human subject, said method comprising:

- (a) detecting RNA encoded by said gene in blood samples of human patients diagnosed as having coronary artery disease, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene in said samples, and/or for cDNA complementary to RNA encoded by said gene in said samples; and
- (b) quantifying a level of RNA encoded by said gene in said samples; and
- (c) comparing said level to a quantified level of control RNA encoded by said gene in blood samples of healthy control subjects;

wherein said gene is a candidate biomarker for coronary artery disease in a human subject if said level of RNA encoded by said gene in said blood samples of said human patients diagnosed as having coronary artery disease is 1.54 times lower than said level of RNA encoded by said gene in said samples of said healthy subjects with a p value equal to 0.0001.

73. (New) The method of claim 71 or claim 72, wherein:

- (i) said blood samples of said human patients diagnosed as having coronary artery disease and said blood samples of said healthy control subjects are whole blood samples; or
- (ii) said blood samples of said human patients diagnosed as having coronary artery disease and said blood samples of said healthy control subjects are blood samples which have not been fractionated into cell types; or
- (iii) said blood samples of said human patients diagnosed as having coronary artery disease and said blood samples of said control subjects are blood samples which comprise leukocytes which have not been fractionated into cell types.

74. (New) The method of claim 71 or claim 72, wherein said quantifying of said level of RNA encoded by said gene is effected by:

- (i) quantifying said level of RNA relative to a housekeeping gene; or
- (ii) quantification of cDNA complementary to RNA encoded by said gene; or
- (iii) using quantitative PCR; or
- (iv) using an array.

75. (New) A method of classifying ATP-binding cassette, sub-family A (ABC1), member 1 (ABCA1) gene expression in a human test subject, said method comprising:

(a) quantifying a level of RNA encoded by said gene in a blood sample of said test subject;

(b) comparing said level in said sample of said test subject with a quantified level of RNA encoded by said gene in blood samples of control subjects classified as having coronary artery disease; and

(c) comparing said level in said sample of said test subject with a quantified level of RNA encoded by said gene in blood samples of control subjects classified as healthy subjects;

wherein a determination from steps (b) and (c) that said level in said sample of said test subject is statistically similar to said level in said samples of said subjects classified as having coronary artery disease and is statistically lower relative to said level in said samples of said subjects classified as healthy subjects, results in a classification of ABCA1 gene expression in said test subject with that of said subjects classified as having coronary artery disease, and wherein a determination from steps (b) and (c) that said level in said sample of said test subject is statistically higher relative to said level in said samples of said subjects classified as having coronary artery disease and is statistically similar to said level in said samples of said subjects classified as healthy subjects, results in a classification of ABCA1 gene expression in said test subject with that of said subjects classified as healthy subjects.